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Mertz, Prema

Sent:

Tuesday, December 20, 2005 12:42 PM

To:

STIC-Biotech/ChemLib

Subject:

10/789,251

Please search SEQ ID NO2 with protein databases.

Please search SEQ ID NO:26 with DNA databases.

Please search SEQ ID NO:2, 26 with US PG PUB databases.

Thanks.

Prema Mertz, Ph.D., J.D.
Primary Examiner
Art Unit 1646
4D81 Remsen Bldg Mailbox 4C70
US Patent & Trademark Office
Tel # (571) 272-0876
FAX # (571) 273-0876

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Searcher:	
Searcher Phone:	_
Date Searcher Picked up:	
Date completed:	
Searcher Prep Time:	
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Ty	ype of Search
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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AD3160
B90153
$64826
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T48023
H84912
E83640
D71302
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72	72	72	72	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	73	73	73	73
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cted by chance to have a of the result being printed, score distribution.  Description  Description  interleukin-10 pre BCRF1 protein - hu interleukin 10 - p interleukin-10 pre interleukin-10 pre Rab geranylgeranyl Rab geranylgeranyl probable beta-adap probable transcrip hypothetical prote hypothetical prote protein kinase CDC hypothetical prote probable membrane hypothetical prote probable synechocy ATP-dependent RNA hypothetical prote probable pro-manNA hypothetical prote probable exomuclea ATP-dependent DNA udp-n-acetylmurama sensory box histid membrane export pr late protein, 100K hypothetical prote hypothetical prote		Search time 16 Seconds thout alignments) 8.384 Million cell updates/sec
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bitory factor (CSIF); IL-10  Reb-1992 #text_change 09-Jul-2004  N.; Johnson, K.E.; Kastelein, R.; Fiorenting, 1991  Cytokine synthesis inhibitory factor cDNA cepMID:1847510  Tanng, R.; Durkin, J.; Baldwin, S.; Paliw. 2000dary structure analysis of human and muri, 2000dary structure analysis of human and muri, 2000min, 2000 per protein  1994  EMBL:U16720; NID:g1041812; PIDN:AAA80104.1; 1994  EMBL:X78437; NID:g1041812; PIDN:AAA80104.1; 1994  EMBL:X78437; NID:g1167482  EMBL:X78437; NID:g1167482  EMBL:X78437; NID:g1167482  EMBL/DDBJ  EMBL/DDBJ  EMBL/DDBJ		hypothetical prote ywbl protein - Bac hypothetical prote variant-specific s hypothetical prote conserved hypothet hypothetical prote conserved hypothet hypothet hypothet hypothetical prote conserved hypothet hypothetical prote

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Interleukin 10 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
C;Accession: I46591

R;Blancho, G.; Gianello, P.; Germana, S.; Baetscher, M.; Sachs, Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995

A;Title: Molecular identification of porcine interleukin 10: regra, Reference number: I46591; MUID:95224028; PMID:7708727

A;Accession: I46591

A;Cession: I46591
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QQBE2
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C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_chang
C;Accession: A03741; S32974
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: cytokine; glycoprotein; lymphokine; T-cell F;1-18/Domain: signal sequence #status predicted <SIG>F;19-178/Product: interleukin-10 #status predicted <MAT>F;30-126,80-132/Disulfide bonds: #status experimental F;34/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P03180; UNIPARC:UPI000000CDBE; EMBL:V01555; NID: R;Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gib Nature 310, 207-211, 1984

A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149

A;Contents: annotation; protein coding region
A; Status: preliminary; translated from
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A; Residues: 1-170 <BAN>
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Pred. No. 1.1e-07;
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                                                                                                                     D.H.; LeGuern,
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                                                                       expression
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RESULT 5 A34853 interleukin-10 |

precursor

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A; Molecule type: mRNA
A; Residues: 1-175 <BLA:
A; Cross-references: UNI
C; Genetics:
A; Gene: I1-10
C; Superfamily: interleu
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A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-179 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <ROD>
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A;Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 ()
A;Reference number: A48558; MUID:93227565; PMID:8385838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S55664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004 
C;Accession: A48558; S55664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names: hypothetical C; Species: equine herpesvirus 2
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                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                  Query Match
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Best Local
                                                                                                                                                                                                                                                                                             Local
                                        156 AAVVKALGELDILLQWME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 LKTLRLRLRRCHQFLPC---ENKSKAVEEVKSAFSKLQ-ERGVYKAMGEFDIFINYIE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 FLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME
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                                                                                                                                                                                                                     39 LOBIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKFANRCCLLRHLLRLYLDRVFKNY
                                                                                                                                                                                                                                                                       44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCV----IATNLQEIRNGFSDIRGSVQA
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                     QAENHSTDQEKDKVNSLGEKLKTLRVRLRRCHRFLPC---ENKSKAVEQVKSAFSKLQ-E
                                                                                                                                  QTPDHYTLR----KISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQ 155
                                                                                                                                                                               LHELRAAFSRVKTFFQMKD-QLD-NMLLDGSLLEDFKGYLGCQALSEMIQFYLEEVMP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDQMGD--LLLTGSLLEDFKGYLGCQALSEMIQFYLEDVMPKAESDGEDIKEHVNSLGEK 111
KGVYKAMSEFDIFINYIE
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Pred. No. 1.1e-07;
4; Mismatches 78
                                                                                                                                                                                                                                                                     Score 147.5; DB 2;
Pred. No. 6.1e-07;
4; Mismatches 59;
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N;Alternate names: cytokine synthesis inhibitory factor (;Species: Rattus norvegicus (Norway rat) C;Date: 30.Sep-1993 #sequence_revision 30.Sep-1993 #text_change (;Accession: JN0475; JC1357; $\overline{S}36021$ R;Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B. Blochem. Biophys. Res. Commun. 192, 452-458, 1992 A;Title: Molecular cloning of rat cytokine synthesis inhibitory: A;Reference number: JN0475 A;Reference number: JN0475 A;Reference nucleic acid sequence not shown A;Rocession: JN0475 A;Rocessio
                                                                                                                      A;Cross-references: UNIPROT:P29456; UNIPARC:UPI0000167959
R;Goodman, R.E.; Oblak, J.; Bell, R.G.
Biochem. Biophys. Res. Commun. 189, 1-7, 1992
A;Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones
A;Reference number: JC1357; MUID:93080542; PMID:1280414
A;Accession: JC1357
A;Molecule type: mRNA
A;Residues: 1,'p',3-64,'L',66-178 <GOO>
A;Feng, L.
R;Feng, L.
submitted to the EMBL Data Library, July 1991 A; Reference number: S36021 A; Accession: S36021
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C;Superfamily: interleukin-10
C;Keywords: cytokine; lymphokine; T-cell
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A;Title: Structure of the mouse II-10 gene and chromosomal localization of the mouse A;Reference number: I56136; MUID:92268508; PMID:1350294
A;Accession: I56136
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A; Residues: 1-178 < RES>
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A; Residues: 1-178 < MOO>
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31.1%; Pred. No. 1.3e-06;
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                                                                                                                                                                GB:L02926; NID:g204903; PIDN:AAA41425.1;
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A;Residues: 1-178 <FE2>
A;Cross-references: UNIPARC:UPI0000167959; EMBL:X60675; NID:GC,Superfamily: interleukin-10
C;Keywords: cytokine; glycoprotein; lymphokine; T-cell F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Product: interleukin-10 #status predicted <MAT>F;29,134/Binding site: carbohydrate (Asn) (covalent) #status
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A; Introns: 1/3;
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A;Title: The genes encoding geranylgeranyl transferase alpha-subunit
A;Reference number: JC5538; MUID:97339427; PMID:9196026
A;Accession: JC5538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-567 <SON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Song, H.J.; Rossi, A.; Ceci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Homo sapiens (man)
;Date: 02-Sep_1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                Query Match
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les 53; Conserv
 479
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                                                                                                                                                                                                                                                      1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE--IRNGFSD---IRGSVQA
                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                               Similarity
                                  EPQAAVVKAL
                                                                                                         YT----LRKISSLANSFLTIK----KDLRLCHAHMTCHCGEEAMKKYSQI-LSH--FEKL
                                                                                                                                             EKSTVLQSELESCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFQTLKAVDPMR
                                                                                                                                                                               KDGNIDIRILRRTESLQDTKPANRCCLLRHLL-----RLYLDRVFKNYQT-----PDH 103
                                                                                                                                                                                                                     LPAASLNDQLPQHTFRVIWTAGDVQK-----ECVLLKGRQEGWCRDSTTDEQLFRCELSV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLOWME 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI 167
                                                                    ATYLDDLRSKFLLENSVLKMEYAEVRVLHLAHKDLTVLCHLEOLLLVTHLDLSHNRLRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLNSLGEKLKTLWIQLRRCHRFLPC---ENKSKAVEOVKNDFNKLODK-GVYKAMNEFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKTFFQKKD-QLDNIVL--TDSLLQDFKGYLGCQALSEMIKFYLVEVMPQAENHGPEIKE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRGSVQAKDGNIDIRILRRTES-LQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLGSALLCCLLLLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATN------LQEIRNGFSD
                                                                                                                                                                                                                                                                                                                                                                                      38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2;
                                                                                                                                                                                                                                                                                            Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%;
 488
                                                                                                                                                                                                                                                                                                                                10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, 235, 10-14, 1997
                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                            Score 94.5; DI
Pred. No. 0.35
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 136; DB 2;
Pred. No. 8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIPARC: UPI000013188E in cutaneous disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GVKT-SKGHSIRGDNNCTHFPVSQTHMLRELRAAFSQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                         DB
.35;
                                                                                                                                                                                                                                                                                            82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transglutamin
                                                                                                         152
                                                                                                                                             418
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45977
R;Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 268, 12221-12229, 1993
A;Title: CDNA cloning and expression of the alpha and beta subunits of rat Rab A;Reference number: A45977; MUID:93280201; PMID:8505342
A;Accession: A45977
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-567 -ARM>
A;Residues: 1-567 -ARM>
A;Residues: 1-567 -ARM>
A;Residues: 1-567 -ARM>
A;Residues: 1-568 -ARM>
A;Residues: 1-569 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable beta-adaptin YKS5 - yeast (Saccharomyces cerevisiae)

NALIternate names: protein G9331; protein YGR261C

C;Species: Saccharomyces cerevisiae

C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004

C;Accession: S64594; S63450

R;Panzeri, L.; Agostoni Carbone, M.L.; Melchioretto, P.; Plevani, P.; Marte; submitted to the Protein Sequence Database, May 1996

A;Reference number: S64591

A;Rocession: S64594

A;Molecule type: DNA

A;Residues: 1-809 <PAN>

A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P46682; UNIPARC:UPI00000530A8; A;Experimental source: strain S288C R;Robinson, L.C.; Engle, H.M.; Panek, H.R. submitted to the EMBL Data Library, September 1995 A;Description: Suppressors of loss of yeast casein kinase 1 A;Reference number: S63439 A;Accession: S63450
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                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SGD:YKS5
A;Cross-references: SGD:S0003493; MIPS:YGR261c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-26, 'PLSWVNPP', 36-723,'T', 725-795,801-809 «
A; Cross-references: UNIPARC: UPI0000168A41; EMBL: U35411;
C; Genetics:
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Best Local S
Matches 46
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Best Local Similarity
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                                                                                                         N
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              EAAAVATSKLGESSYTYY--SQNINPQQLVTLLNSRNSREVRDAMKRIISIMASDDDSID
                                                                                                         KASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNID
                                                                                                                                                                                                                                                                                                                                                                                           ZR
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                                                                                                                                                                                                     39;
                                                                                                                                                                                                Score 93.5; DB 2;
Pred. No. 0.66;
9; Mismatches 73;
                                                                                                                                                                                                     73;
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                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g1017728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function
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                   78
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probable transcription regulator PA4135 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: F83128 C;Accession: F83128 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb
                                                                                                                                                    A;Residues: 1-646 <JOHS
A;Cross-references: UNIPROT:O76579; UNIPARC:UPI0000076553;
A;Cross-references: strain Bristol N2; clone C16A11
                                                                                                                                                                                                                                                                                                                       R;Johnson, D.; Biewald, T. submitted to the EMBL Data Library, July 1998 A;Description: The sequence of C. elegans cosmid C16All.
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C16A11.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T33346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-140 <STO>
A;Cross-references: UNIPROT:Q9HWP6; UNIPARC:UPI00000C5C2C;
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A82950;
A;Accession: F83128
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Molecule type: DNA
                                                                                                                           A;Gene: CESP:C16A11.5
                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                 A; Accession:
                                                                                                                                                                                                                                                                                                   A; Reference number:
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Matches
Matches
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rons: 35/3; 72/1;
                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ---FLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 DSNSELR-CFA--LSALSDMKMSSLAPTILHTVKKLVTDPSAMVRGEVALATIKLYRAGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TIKKDLRLCHAHMTCHCGEBAMKKYSQILSHFEK---LEPQA-----AVVK--ALGE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 QQCFVSMSGDMEKNYQRIQERFGEEKLAQLLELLNELKKIKP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IRILRQQGEMESYQLANQACILRPSMTGVLARLERDGIVRRWKAPKDQR-RVYVNLTEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 IRILARTESLODTKPANRCCLLRH-----LLRLYLDRVFKNYQTPDHYTLRKISSLANS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 VQLYFADVVKNITTNDTK------VKRLIHLYLLRFAEN---DPNLTLLSINSLQKSLS
Similarity
36; Conserv
                                                                                                                                                                                                                                                                                 T33346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LDILLQWMEETE 176
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Conservative
                                                                                                                                                                                                                                                                                                     Z21328
                                                                              94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2;
               9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337; PMID:10984043
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22;
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Pred. No.
                      Score 81.5;
Pred. No. 7
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Mismatches
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                                          DB 2;
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49;
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                                      Length 646;
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  Indels
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                                                                                                                                                                                              EMBL: AF077536;
  31;
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A.; Larbig,
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                                                                                     540/2;
                                                                                                                                                                                              PIDN:AAC26261
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K.; Lim,
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RESULT 13
T19925
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A;Residues: 1-1062 <SAU>
A;Cross-references: UNIPARC:UPI0000127259; EMBL:AL035537; PIDN:CAB36886.1; GSPDB:GN0006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P41892; UNIPARC:UPI0000127259; EMBL:X78799; A;Experimental source: wildtype 972 h minus A;Note: mRNA sequencing was also done confirm the intron borders R;Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, February 1999 A;Reference number: Z21860
                                          hypothetical protein C44C10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T19925
R;Cottage, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19197
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EMBO J. 13, 301-3019, 1994
A;Title: The cdc7 protein kinase is a dosage dependent regulator
A;Reference number: S46367; MUID:94313982; PMID:8039497
A;Accession: S46367
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S46367
  A; Reference number:
A; Accession: T19925
A; Status: prelimina:
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A;Introns: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 972h-; cosmid c21
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A; Residues: 1-1062 < FAN>
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: ATP; cell division, phosphotransferase, protein kinase;7-259/Domain: protein kinase homology <KIN>;1-23/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                            LLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%;
ilarity 30.2%;
Conservative 2
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                                                                                                                                 #sequence_revision 15-Oct-1999 #text_change
  translated
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Pred. No. 15;
20; Mismatches
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from
  GB/EMBL/DDBJ
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2-isopropylmalate synthase, probable (leuA-1) [imported] - C;Specias: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_ch C;Accession: B90153
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B90153
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A; Gene: CESP:C44
A; Map position:
A; Introns: 66/3;
                                                                                                                                                                                                                                                               A;Gene: g.
A;Genome:
                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wood, D.W.; Setubal, J.C.; Kaul, R. erage, G.; Gillet, W.; Grant, C.; Gue; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle,
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A;Residues: 1-542 <WIL>
A;Residues: 1-542 <WIL>
A;Cross-references: UNIPROT:Q18616; UNIPARC:UPI000017B837; EMBL:Z69787;
A;Experimental source: clone C44C10
C;Genetics:
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A;Cross-references: UNIPROT:Q9WWF4; UNIPARC:UPI0000D146D;
A;Experimental source: strain C58 (Dupont)
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24.6%; Pred. No. 17;
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23.2%; Pred. No.
                           LRLYLDRVFKNYQT-PDHYTLRKISSLANSFLTIKK 121
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, Guenthner, D.; Kutyavin,
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24-May-2001 #text\_change 09-Jul-2004

Sulfolobus solfataricus

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A,Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: B90153

A;Status: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Rolecule type: DNA
A;Cross-references: UNIPROT:Q980Z1; UNIPARC:UPI000006418D; GB:AE006641; NID:g13813259; F. C;Genetics:
A;Gene: leuA-1
C;Superfamily: 2-isopropylmalate synthase leuA
Search completed: December 24, 2005, 10:28:05 Job time : 18 secs
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## **Protein Sequence Searches - February 2005**

. All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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9; F G.D., N.K.,	rush J., Dowd P., sld J., gld J., gls A., dard A.D., cale teins: a	., vi Q.,	.)00187-8; Haugen H., lk J., e in	Zcyto10). stomi; Hominidae;		oryctolagus oryctolagus oryctolagus equine herp equine herp mus musculu homo sapien sigmodon hi trichosurus trichosurus equus cabal bubalus bub cercopithec bos taurus saimiri sci canis famil

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.":
PROSITE; PS003520; IN Cytokine; Direct pro. SIGNAL 1 CHAIN
                                                                                                        HSSP; Q9UHDO; INIF.
ENSGMD1; ENSGG0000162891; H
HGNC; HGNC:6002; II20.
MIM; 605619; -
GO; GO:0005576; C:extracell
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I- FUNCTION: Cytokine that may be psoriasis. Acts through STAT3.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed at
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c. Natl. Acad. Sci. U.S.
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MGI; MGI:1890473; Il20.

GO:0005615; C:extracellula;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 109:3-13 (Cytokine that may be involved a psoriasis. Acts through STAT3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-10 family.
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Cell 104:9-19(2001).
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GO:0045517; F:interleukin-20 receptor binding; IDA.

GO:0040517; F:hemopoies1s; NAS.

GO:0040506; P:positive regulation of epidermal cell diffe.

GO:0045618; P:positive regulation of keratinocyte differe.

GO:0042517; P:positive regulation of tyrosine phosphoryla.

GO:0050727; P:regulation of inflammatory response; ISS.

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                                                                                                                                                                                                                                                                                                       -; mRNA
                                                                                                                                                                                                                                                                 Mus musculus.
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-> S (in Ref. 3)
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MBL outstation -
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Best Local Sim
Matches 131;
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NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Liao Y.-C., Liang W.G., Chen F.W., Hsu

"IL-19 induces production of IL-6 and
apoptosis through TNF-alpha.",
J. Immunol. 169:4288-4297(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                             Conklin D., Petersen J.,
Sexson S., Smith D., Lok
"Homo sapiens homolog of
Submitted (OCT-1999) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE:
MEDLINE=21040165; PubMed=11196675; DOI=10.1038/sj.gene.6363714;
Gallagher G., Dickensheets H., Eskdale J., Izotova L.S.,
Mirochnitchenko O.V., Peat J.D., Vasquez N., Pestka S., Donnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Interleukin-19 precursor (II-19) (Melanoma differentiation protein-like protein) (NG.1).
Name=IL19; Synonyms=ZMDA1;
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Q9UHDO; Q96
                  Rieder M.J.,
Nickerson D.
                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes
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Eukaryota; Metazoa;
                                                         NUCLEOTIDE
                                                                                                                        Kotenko
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, expression and initial characterization of interleukin-19 (IL-19), a novel homolog of human interleukin-10 (IL-10)."; Genes Immun. 1:442-450(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kotenko S.V.;
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.V., Pestka
(JUN-2001)
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                                    SEQUENCE [GENOMIC DNA], AND VAR., Carrington D.P., Chung M.-W.,
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  program
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Pred. No. 1.5e
L5; Mismatches
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Potential.
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TNF-alpha and
                                                           VARIANT
  genomic
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.5e-57;
                                        Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                             tion associated databases.
                                                                                                  databases
                                      K.L.,
                                                           PHE-175
applications,
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                                    Poel C.L.,
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MKLQCVSLWLLGTILILCSVDNHGLR-----RCLISTDMHHIEESFQEIKRAIQAKDTFP MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 69;

36;

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GO; GO:0005125; F:cytokine activity; TAS:
GO; GO:0006955; P:immune response; NAS:
GO; GO:0007165; P:signal transduction; NI
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR012351; InterleuKin_10.
Pfam; PR00726; II10; 1.
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                                                                                                                                                                      Glycoprotein;
SIGNAL
CHAIN 2
CARBOHYD 5
CARBOHYD 13
DISULFID 7
DISULFID 7
VARIANT 17
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                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG000001422
HGNC; HGNC:5990; IL19.
MIM; 605687; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00520; INTERLEUKIN 10;
3D-structure; Apoptosis; Cytokine;
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-!- SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BL; AF276915; AAG16755.1; -; Genomic_DNA.
BL; AF453946; AAN40906.1; -; mRNA.
BL; AF192498; AAF06663.1; -; mRNA.
BL; AY040367; AAK91776.1; ALT_INIT; mRNA.
BL; AY30905; AAK64498.1; -; Genomic_DNA.
BL; AL049615; CAB72342.1; -; Genomic_DNA.
B; INIF; X-ray; A=19-177.
B; INIF; X-ray; A=19-177.
B; INIF; X-ray; A=19-177.
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FUNCTION: May play some important
Up-regulates IL-6 and TNF-alpha an
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                                Similarity
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Polymorphism;
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international sequencing consortium;
) to the EMBL/GenBank/DDBJ databases
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Score 337.5; 1
Pred. No. 9.4e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                    S -> F.
/FTId=VAR 013077.
; 7CCFAC22177DE408
                                                                                                                                                                                                                                                                                       Interleukin-19.
N-linked (GlcNAc.
N-linked (GlcNAc.
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s apoptosis (F
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RESULT 4
QSVUT3 HUMAN
ID QSVUT3;
AC QSVUT3;
DT 01-FEB-2005 (T
RP NUCLEOTIDE SE(
RA KAY M.;
CC -1-SUBCELLULJ
DR KAY M.;
CC -1-SUBCELLULJ
DR SMR; QSVUT3;
DR Ensembl; ENSGI
DR GO; GO:000515
DR GO; GO:000595
DR INTETPO; IPR
DR GFAM; PF00726
DR PFAM; PF0726
DR PFAM; PF0726
DR PFAM; PF0726
DR CYTOKING.
QALDRA BE OUT OF ALL PARTS OF A
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Best Local S
Matches 69
                                                                             13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Interleukin 10 family protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Actinopterygii, Neopterygii, Teleostei, Ostariophysi
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ datal -! - SUBCELLULAR LOCATION; Secreted (By Similarity) EMBL, AL513315; CAH71814.1; -; Genomic_DNA. SMR; Q5VUT3; 60-215.
Ensembl; ENSGO0000142224; Homo Sapiens.
G0; G0:0005615; C:extracellular space; IEA.
G0; G0:00055125; F:cytokine activity; IEA.
G0; G0:00055125; F:cytokine activity; IEA.
                                                                                                                                                                                                                                               Q4LDR4 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000098; Pfam; PF00726; IL10;
    NUCLEOTIDE SEQUENCE.
Ram S., Daisuke I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IL19; ORFNames=RP11-262N9.2-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIRILARTESLODTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 AA;
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      Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24567 MW; D79D6B0F11DA74E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.1%;
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Last sequence update)
Last annotation updat
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Pred. No. 1.2
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                                                                                                      Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
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                                                                                                                           Euteleostomi;
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Best Local (
                                                                                                                         Ensembl; ENSMUSG00000016524; Mus musculus.

MGI: MGI: 1890472; Il19.

GO: GO:0006917; P:induction of apoptosis; IDA.
GO: GO:004226; P:interleukin-6 biosynthesis; IDA.
GO: GO:004226; P:oxygen and reactive oxygen spec
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR000098; Interleukin_10.
ProDom; PD003687; Interleukin_10; 1.
SMART; SM00188; IL10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q8CJ70;
10-MAY-2005
        CARBOHYD
CARBOHYD
                                                                 Apoptosis;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Up-regulates II-6 and TNF-alpha and induces apoptosis.

Up-regulates II-6 and TNF-alpha and induces apoptosis.

ISUNCELULIAR LOCATION: Secreted.

ISUNITARITY: Belongs to the II-10 family.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22257669; PubMed=12370360;
Liao Y.-C., Liang W.G., Chen F.W., Hsu
"IL-19 induces production of IL-6 and
apoptosis through TNF-alpha.";
J. Immunol. 169:4288-4297(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Euarchontogl
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Evolution of IL-10 family genes in teleosts"; Submitted (JUL-2005) to the EMBL/GenBank/DDBJ da EMBL; AB219579; BAE06181.1; -; mRNA. SEQUENCE 168 AA; 19110 MW; 807D18AD736C709B
                                                                                                                                                                                                                                                                                                                                 EMBL; AF453945; AAN40905.1; HSSP; Q9UHDO; 1N1F.
                                                                                                                                                                                                                                                                                                                                                                                                                 use
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STRAIN=Swiss Webster /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-19
Name=Il19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Interleukin-19 precursor (IL-19).
                                                                                                                                                                                                                                                                                                            SMR; Q8CJ70; 23-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                           PROSITE; PS00520;
                                                                                                                                                                                                                                                                                                                                                                                              removed
                                                                                                                                                                                                                                                                                                                                                                                                                   89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANRCCLLRHLLRLYLDRVFKNYQTFDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWDAAQG-RRLHLGSCKVNIHTHELRHHFQYVRQGMISGDDHKGIRLLRKDVMSSLQATE
                                                                                      Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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25
56
127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                      INTERLEUKIN_10; FALSE
        24
176
56
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%;
                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                      <u>.</u>!
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Pred. No. 1.1e-21;
        Interleukin-19.
N-linked (GlcNAc.
N-linked (GlcNAc.
                                                                   Potential
                                                                                                                                                                                                                                                                                                                                                                                                                   in no way
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                                                                                                                                                                                                                                                                                                                                                        mRNA.
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                                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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I TNF-alpha
                                                                                                           NEG
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pha and
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Sciurognathi;

×-S cell

(Potential). (Potential).

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                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative genomic analysis reveals independent expansion of
Ilneage-specific gene family in vertebrates: The class II cytok
T receptors and their ligands in mammals and fish.";

BMC Genomics 4:29-29(2003).

R EMBL; AY294557; AAP57416.1; -; Genomic_DNA.

EMBL; AY294558; AAP57416.1; -; Genomic_DNA.

R GO; GO:0005615; C:extracellular space; IEA.

R GO; GO:0005125; F:cytokine activity; IEA.

R GO; GO:0005955; P:immune response; IEA.

R GO; GO:0006955, P:immune response; IEA.

R InterPro; IPR010351; Cytokine 4 hlx.

R InterPro; IPR010351; Cytokine 4 hlx.

R FADDom; PD003607; Interleukin_10.

R Pfam; PF00726; IL10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                         ProDom;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q75X60
Q75X60,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
PubMed=12869211; DOI=10.1186/1471-2164-4-29;
Lutfalla G., Crollius H.R., Stange-Thomann N.,
Mogensen K., Monneron D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=IL20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETNG
                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
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                                                                           83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                            SM00188; IL10; 1
                                                                                                                                                                                                                                                                      57,
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%;
Similarity 38.6%;
56; Conservative :
QILSHFEKLEPQAAVVKALGELDILLQMME 173
                                                                      CTLLVDSCSISADLQEWHQHHSNIRLNAITEDEEIGVKLLSK-RLMEDVQDGQRCCFLRL
                                                                                                                                                                                                                  KTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNQLEVSSAALKSLGELNILLAWID 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEKLEPQAAVVKALGELDILLOWME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYRDRVFQDHQERSLEVLRRISSIANSFLCVQKSLERCQVHRQCNCSQEATNATRIIHDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLDRVFKNYQTPDHYTLRKISSLANSPLTIKKDLRLCHAHMTCHCGEBAMKKYSQILSH
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                                                                                                                                                                                                                                                                                                                                                                175 AA;
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                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
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120
126
128
20288
                                                                                                                                                                                                                                                                                                                                                                   19838 MW;
                                                                                                                                                                                                                                                                                          29.3%; Score 266.5; DB 2 38.0%; Pred. No. 8.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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By similarity.
By similarity.
By similarity.
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Pred. No. 2.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y similarity.
by similarity.
by similarity.
73B6C1BC54077FDC (
                                                                                                                                                                                                                                                                                                                                                                   DE6FA67E0038E034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                              <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytokine
                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                    Gape
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RESULT 9
Q92584 MOUSE
ID 592584;
AC Q92584;
DT 01-DEC-2001 (T
DT 01-DEC-2004 (T
DT 01-MAR-2004 (T
DE Melanoma diffe
GN Mus musculus (
OC Eukaryota; Met
OC Muridae; Murin
OX NCBI_TaxID=100
RN [1]
RN NUCLEOTIDE SEC
RP MIGHETED SEC
RC STRAIN=129/SvJ
RA Madireddi M.T.
Submitted (FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
1925/J
1025/J
10
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Best Local :
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/3 MOUSE
Q925J3
^925J3
NUCLEOTIDE SEQUENCE.
STRAIN=129/SvJ;
Madireddi M.T., Lin J.,
Submitted (FEB-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
Cytokine.
SEQUENCE
                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
Muridae; Murinae; M
                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
Melanoma differentiation associated gene-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINB=21240641; PubMed=11342597;
Schaefer G., Venkataraman C., Schindler U.;
Schaefer G., Venkataraman C., Schindler U.;
"PISP (IL-4-induced secreted protein), a novel cytol
secreted by Th2 cells.";
J. Immunol. 166:5859-5863(2001).
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; AF333251; AAK52470.1; -; mRNA.
                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD003687; Interleukin_10; SMART; SM00188; IL10; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensembl; ENSMUŚGO0000026420; Mus muscu: MGI; MGI;2135548; I124.
GO:00056515; C:extracellular space; InterPro; IPR000098; Interleukin_10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Th2-specific cytokine FISP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00520; INTERLEUKIN_10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLDAFNKLEASKAVLKAVGELDTVLQWLQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                     Euarchontoglires;
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                                                                                                                                                                                                                  Chordata;
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26,
          Su ;
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          Z., Shay J.W., Huberman E., I
EMBL/GenBank/DDBJ databases
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 222;
Pred. No. 2
                                                                                                                                                                             Craniata; Vertep
oglires; Glires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5BF76C8612AC909D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-13
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                                                                                                                                                                                       Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brata; Euteleostomi;
Rodentia; Sciurognathi;
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Best Loc
Matches
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Q13007; Q95DB0; Q96KG4;
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Interleukin-24 precursor (Suppression of tumo
(Melanoma differentiation-associated protein
                                                                                                                                                                                                                                                                                                                                           TISSUB-Melanoma;
MEDLINE-9613269; PubMed-8545104;
MINE-9613269; PubMed-8545104;
Jiang H., Lin J.J., Su Z.-Z., Goldstein N.I., F
"Subtraction hybridization identifies a novel m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF235006; AAK52590.1; -; mRNA. Ensembl; ENSMUSG00000026420; Mus muscul MGI; MGI:2135548; I124.
GO; GO:0005615; C:extracellular space; InterPro; IPR000098; Interleukin_10.
                                                                                                                         Madireddi M.T., Lin J., Su Z.-Z., Shay J.W., Huberman E., F. Genomic structure, chromosomal localization and expression melanoma differentiation associated gene-7 (mda-7): potentia relationship with cellular senescence.
                                                                                                                                                                                                                                     Peat J., Kube D., Eskdal "The human MDA-7 gene."; Submitted (JUN-2000) to
                                                                                                                                                                                                                                                                                                                  associated gene, mda-7, modulated during h differentiation, growth and progression."; Oncogene 11:2477-2486(1995).
              Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K. Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; "SeattleSNPs NHLBI HL66682 program for genomic applications,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00520; INTERLEUKIN_10; 1.
Cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                         TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=IL24; Synonyms=MDA7, Homo sapiens (Human).
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                                                                                NUCLEOTIDE
                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND VARIANT HIS-124.
                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00188; IL10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD003687; Interleukin_10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPISESAHORFLLFRRAFKQLDTEVALVKAFGEVDILLTWMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD
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                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                    Eskdale J., Jueliger
                                  T.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20812 MW; 05CA43872D53D555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                [GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%;
                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ
                                                                                                               the
                             Carrington D.F
Q., Nickerson
http://pga.gs.washington.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted (By similarity).
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                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 220;
Pred. No. 3.
                                                                             DNA], AND
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                                                 D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n of tumorigenicity protein 7) (MDA-7).
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                                                                                VARIANTS
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es 71; Indels
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                                                                                                                                                                                                                                                                      Gallagher
                                                                                                                                                                                                                                                                                                                                                                  Fisher P.B.; melanoma differentiation
                                                                                                               databases
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                                                                                                                                                                                                                                                                                                                                                     melanoma
                                                                              HIS-124;
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                                               3. -W.,
                                                                                                                                           potential
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                                                                                ARG-125
                                                                                                                                                                          Fisher P.B.;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Dedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9904569; PubMed=9926712; DOI=10.1073/pnas.95.24.14400;
A Su Z.-Z., Madireddi M.T., Lin J.J., Young C.S.H., Kitada S.,
A Reed J.C., Goldstein N.I., Fisher P.B.;
A Reed J.C., Goldstein N.I., Fisher P.B.;
T'The cancer growth suppressor gene mda-7 selectively induces apoly
T'in human breast cancer cells and inhibits tumor growth in nude m.
Proc. Natl. Acad. Sci. U.S.A. 95:14400-14405(1998).

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Proc. Natl. Acad. Sci. U.S.A. 95:14400-16405(1998).

Proc. Natl. Acad. Ac
                                                                                                                                                                                                                                Ensembl; ENSG00000162892; HGNC; HGNC:11346; IL24. H-InvDB; HIX0001532; -.
                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; "Signal peptide prediction based on analy verified cleavage sites."; Protein Sci. 13:2819-2824(2004).
                                                                          InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR002098; Interleukin 10.
ProDom; PD003687; Interleukin 10; 1.
SMART; SM00188; IL10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2001) to the [5]
                                                                                                                                                                                                        MIM;
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Apoptosis; Cy Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                  PROSITE; PS00520;
                                                                                                                                                                                GO; GO:0006915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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                                                                                                                                                                                                                                                                                 U16261; AAA91780.1; -; mRNA.
AF276916; AAG41401.1; -; Genomic_[
AF235005; AAK52589.1; -; Genomic_[
AY062931; AAL34146.1; -; Genomic_[
BC009681; AAH09681.1; -; mRNA.
bl; ENSG00000162892; Homo sapiens.
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                          Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content is in
  Signal
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NCBI_TaxID=9606;
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13-SEP-2005
13-SEP-2005
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                                                                                                                                                                          Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; BT007156; AAP35820.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                            77 HUMAN
Q53XZ7 HUMAN PRELIMINARY;
Q53XZ7;
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                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                      Similarity
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                   RILQQ-EVIQNVSDAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIV
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KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE
                                  RILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY--QTPDHYTLRKISSLANSFLTIK
                                                               LGFTL-----LLWSQVSGAQGQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNITSA
                                                                            LAFSLLSAAFYLLWTPSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVQAKDGNIDI
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/FTId=VAR (11974.

H -> R (in dbsNP:3093431).

/FTId=VAR 013097.

V -> L (in dbsNP:3093446).
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Last sequence update)
Last annotation updat
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Pred. No. 7.3e-13
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SEQUENCE
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J. Biol. Chem. 275:24436-24443(2000).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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-!- SIMILARITY: Belongs to the IL-10 family.
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76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 191;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine-like protein Mob-5. N-linked (GlcNAc. . .) (Pote
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2.2e-10;
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Q9WVP8; Q9WVP8; 01-NOV-1999 01-NOV-1999 01-MAR-2004

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

12, 12, 26,

Created)
Last sequence update)
Last annotation update)

PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cutaneous rat wounds express c49a, a novel gene with human melanoma differentiation associated gene, mda-7.
J. Cell. Biochem. 74.1-10(199).

-1- SUBCELLULAR LOCATION: Secreted (By similarity).

EMBL; AF004774; AAB69171.1; -; mRNA.
GO; GO:0005176; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005125; P:immune response; IEA.
InterProj. JPR000098; Interleukin_10.
PROSITE; PS00520; INTERLEUKIN_10; 1.
PROSITE; PS00520; INTERLEUKIN_10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
          Rothwell L., Young J., Zoorob R., Whittaker Rarcher A., Smith A.L., Kaiser P.; "Cloning and Characterization of Chicken IL Immune Response to Eimerla maxima."; J. Immunol. 173:2675-2662(2004).
J. Immunol. 173:2675-2662(2004).
EMBL; AJ621254; CAF18432.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:006955; P:immune response; IEA.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR012352; IL-10 add helix.
InterPro; IPR012352; IL-10 add helix.
InterPro; IPR012352; III-10 add helix.
                                                                                                                                                                                                                                                                                                                            Q6A2H5;
25-OCT-2004
25-OCT-2004
25-OCT-2004
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordatae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley;

MEDLINE-9930986; PubMed=10381256;

DOI=10.1002/(SICI)1097-4644(19990701)74:1<1::AID-JCB1>3.3.CO;2-D;
Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
Chiu R., Tieu A., Ting K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                Interleukin-10.
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                                                                                                                                                                                                                                                                                                                                                                                                     _CHICK
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47; Conserv
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Last annotation updat
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Pred. No. 5.
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                                                                                                                                                                               Whittaker C.A.,
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mda-7.";
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Q6A2H4 CHICK
ID Q6A2H4;
ID Q6A2H4;
AC Q6A2H4;
DT 25-OCT-2
DT 25-OC
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Best Local
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immune Response to Eimeria maxima.";
J. Immunol. 173:2675-2682(2004).
EMBL; AJ621614; CAP21727.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006915; F:immune response; IEA.
InterPro; IPR01235; Cytokine 4 hlx.
InterPro; IPR012352; IL-10 add helix.
InterPro; IPR012352; IL-10 add helix.
InterPro; IPR012352; IL-10 add helix.
InterPro; IPR012352; III-10 add helix.
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                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00726; IL10; 1
PRINTS; PR01294; INTRLEUKIN10.
ProDom; PD003687; Interleukin 10;
SMART; SM00188; IL10; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1294; INTRLEUKINIO.
ProDom; PD003687; Interleukin_10;
SMART; SM00188; IL10; 1.
SEQUENCE 175 AA; 20514 MW; B0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rothwell L., Young J., Zoorob R., Whittal Archer A., Smith A.L., Kaiser P.; "Cloning and Characterization of Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6A2H4_CHICK PRELIMINARY;
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                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                               SM00188; IL
E 175 AA;
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KATIRRCHRFFTC---EKRSKAIKQIKETFEKMD-ENGIYKAMGEFDIFINYIEE
                                                  KKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE
                                                                                                                                                     IDIRILARTESIODTKPANRCCLLRHLIRLYLDRVFKNYQTPDHYTLRKISSLANSFLTI
                                                                                                                                                                                                          MQTCCQALLLLLAACTL--
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                                                                                                     LNIQLL-SSELLDEFKGTFGCQSVSEMLRFYTDEVLPRAMQTSTSHQQSMGDLGNMLLGL
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28,
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                                                                                                                                                                                                             -PAHCLEPTCLHFSELLPARLRELRVKFEEIKDYFQSRDDE
                                                                                                                                                                                                                                                                                                          Score 175.5; DB
Pred. No. 7e-09;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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Search completed: December 24, 2005, 10:31:59 Job time: 230 secs

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-MODEL-frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10789251/runat_23122005_152435_19747/app_query.fasta_1.327
-Q=/cgn2 1/USPTO_spool_p/US10789251/runat_23122005_152435_19747/app_query.fasta_1.327
-Q=/cgn2 1/USPTO_spool_p/US10789251/runat_23122005_152435_19747/app_query.fasta_1.327
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.xge -MINMATCH=0.1 -LÖOPCL=0 -LÖOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALION=200 -THR_SCORRE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10789251_@CGN 1 1 7415 @xinat 23122005 152435_19747 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## ALIGNMENTS

	7297	BD087297 926 bp DNA linear PAT 27-AUG-2002
S ISM	NOIS	BD087297 BD087297.1 GI:22632907
AL ISM	)RDS	JP 2001524313-A/1.
AL RS	ANISM	Homo sapiens (human) Homo sapiens
CE 1 () RS Comman AL Pater ZYMOX OS PN PD PF PR PR PI C12N1 A61P1 PC		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
RS CONkl Mamma Pates ZYMOO OS PN PD PD PF PR	ENCE	1 (bases 1 to 926)
AL Pater ZYMOO OS PN PD PF PF PF PF PR	HORS	Conklin, D.C., Haldeman, B.A. and Grossmann, A.
ZYMOC OS PN PD PF PF PR C12N1 A61P1 PC	RNAL	Mammalian cytokine-like polypeptide-10 Patent: JP 2001524313-A 1 04-DEC-2001:
OS PN PD PF PR PI C12N1 A61P1 PC PC		ZYMOGENETICS INC
PN JF 2001524313-A/1 PD 04-DEC-2001 PD 04-DEC-2001 PF 25-NOV-1998 JF 2000522245 PF 26-NOV-1998 JF 2000522245 PR 26-NOV-1997 US 08/979156 PT DARRELL C CONCLIN, BETTY A HALDEMAN, ANGELIKA GROSSMANN PC C12N15/09, A01K67/027, A61K38/00, A61K48/00, A61P1/02, A61P1/00, PC A61P37/00, A61P37/02, A61P43/00, C07K14/52, C07K16/24, C07K16/42, PC C12N15/00,	T	
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		C12N15/09,A01K67/027,A61K38/00,A61K48/00,A61P1/02,A61P11/00, PC A61P17/00,

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                                    Conklin, D.C., Haldeman, B.A. and Grossmann, Mammalian cytokine-like polypeptide-10 Patent: EP 1424393-A 1 02-JUN-2004;
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                            Zymogenetics Inc
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                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
Hominidae; Homo.
Moore,M.D.
Anti-il-20 receptor antibodies using in inflammation
                                            Xu, W., Kindsvogel, W.R. Dillon, S.R., Lehner, J.
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| GAGGAGACAGAA
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Homo sapiens four alpha helix
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Conklin,D.C. and Haldeman,B.A.
Mammalian cytokine-like polypeptide-10
Patent: US 6576743-A 1 10-JUN-2003,
ZymoGenetics, Inc., Seattle, WA
        1 (bases 1 to 926)
Blumberg, H., Conklin, D., Xu, W.F., Grossmann, A., Brender, T., Carollo, S., Eagan, M., Foster, D., Haldeman, B.A., Hammond, A., Haugen, H., Jelinek, L., Kelly, J.D., Madden, K., Maurer, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                        Hominidae; Homo
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           Homo sapiens
                                                                                                                             AF224266.1 GI:7109206
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Parrish-Novak,J., Prunkard,D., Sexson,S., Sprecher,C., Waggie,K.,
                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                      | GluGluThrGlu
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Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
Homo sapiens four alpha helix cytokine allele 1
Unpublished
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Interleukin 20: discovery, receptor identifica epidermal function Cell 104 (1), 9-19 (2001)
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Conklin,D., Grossmann,A.,
Direct Submission
GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet
                                                                                        HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu
                                                                                                                                                                      AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys
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/product="four alpha helix cytokine"
/protein id="AAF36679.1"
/db_xref="GI:7109207"
/db_xref="GI:7109207"
/tranalation="MKASSLAPSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
GFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                                                                   GGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods for enhancing expression of recombinant proteins Patent: WO 2005058946-A 18 30-JUN-2005;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                    HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
                                               GAGGAGACCGAA 459
                                                                                    GluGluThrGlu
                                                                                                                               GAACCGCAGGCAGTGGTGAAAGCTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG
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                                                                                                                                                                                                               CACTGTGGTGAGGAAGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG
                                                                                                                                                                                                                                                                                            GCCAACTCCTTGACCATCAAAAAAAGACCTGCGTCTGTGTCACGCCCACATGACCTGC
                                                                                                                                                                                                                                                                                                                          AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
                                                                                                                                                                                                                                                                                                                                                                              CGTGTTTTCAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTACCGAGTCTCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CygVallleAlaThrAgnLeuGlnGluIleArgAgnGlyPheSerAgpIleArgGlySer 20
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AUTHORS
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IMAGE:7262116), complete c
BC069311
BC069311.1 GI:47480994
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing o
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-APK-2004) National Institutes of Gene Collection (MGC), Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRBR Plate: 1 Row: c Column: 2.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Kowis, C.R., Sneed, A.J., Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                      Gibbs, R.A.
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                                                                                 pPCR-Script Amp SK(+) "
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                     IL10D, IL-20, MGC96907"
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Best Local Similarity:
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1 (bases 1 to 531)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                    Homo sapiens interleukin IMAGE: 7262128), complete
                                                                                           Homo sapiens
                                                                                                                                         BC069364.1 GI:47479475
                                                Hominidae;
                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysVallleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
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                                                                                                                                                                                                                                                              GAGGAGACAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrígues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodríguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and monice china secuences
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Direct Submission

Submitted (29-APR-2004) National Institutes of Health, Mammalian Submitted (29-APR-2004) National Institute, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer 
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Location/Qualifiers
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Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
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COntact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Gibbs, R.A.
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D.M., Nanavati,
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KEYWORDS
SOURCE
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DB:
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E 1 (bases 1 to 531)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Mammalia; Eutheria;
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**& B 8** 

ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln

CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer

156

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JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSRTM
TITLE
                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REMARK
COMMENT
US-10-789-251-26 (1-144) x BC069398 (1-531)
                                                                                                                                           Score:
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TITLE
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Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
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Center code: BCM-HGSC
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GFSEIRGSVQAKOGNIDIR ILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
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12 (bases 1 to 53)

13 (bases 1)

14 (bases 1)

15 (collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Gasavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Wadan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

18 Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse CNNA semiences
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                                                                                                                           Director MGC Project.

Direct Submission

Submitted (29-APR-2004) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor H
                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                    ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
                                                                                                                                                                                         CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center Center code: BCM-HGSC
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/tissue type="PCR rescued clones"
/clone\_Tib="NIH\_MGC\_244" note="Vector: pPCR-Script Amp SK(+)" precursor" IL10D, IL-20, MGC96907"

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El 1 (bases | to 531)

RS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

TM Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
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                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRBR Plate: 1 Row: 9 Column: 2.
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Submitted (29-APR-2004) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
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Sequencing Center
                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Baylor Human Genome Sequencing Center
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Tissue Procurement: Baylor Hu
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Contact: MGC help desk
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Mammalia; Eutheria;
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                                                                                                                                                             Gibbs, R.A.
                                                           Location/Qualifiers
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Query Match:
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  Homo sapiens interleukin IMAGE:7262176), complete BC069487 BC069487.1 GI:47480770
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                                                                                                                                                           GAGGAGACAGAA
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Indels:
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                                                           linear
clone MGC:
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156 20

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JOURNAL
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AUTHORS
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El (Dases 1 to 531)

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McSwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McSwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McSwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Villalon E, Ketteman M, Madan A, Gay LJ, Hulyk SW, Villalon E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Gereen ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Kzzywinaki MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdha/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Baylor Human Genome Sequencing Constitution (LLNL) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC
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the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Location/Qualifiers
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                                                                                                                                                               gene="IL20"
                                                                                                                                                                                                                                                                                                                                                                                              note="Vector:
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ALGELDILLQWMEETE"
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## KEYWORDS SOURCE ORGANISM RESULT 14 BC069523 밁 Percent Similarity: Best Local Similarity: Query Match: Ś 밁 Ş 밁 Ś 밁 Ş 밁 Ś Ś 문 ş 밁 REFERENCE US-10-789-251-26 (1-144) x BC069487 Score: VERSION ACCESSION DEFINITION Alignment Snoo AUTHORS No:: 517 397 337 277 157 141 GluGluThrGlu 144 457 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 101 217 81 13 41 97 21 Hominidae; Homo. 1 (bases 1 to 531) 1 (bases 1 to 531) Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Strausberg RL, Feingold EA, Grouse LH, Derge JG, Altschul SF, Zeeberg Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Heieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Homo sapiens interleukin IMAGE:7262093), complete Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens Homo sapiens (human) BC069523.1 GI:47479431 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGT CysVallleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer GAGGAGACAGAA 528 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 4.73e-72 749.00 100.00% 99.31% 99.47% Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; (1-531)531 bp mRNA linear PRI 20, mRNA (cDNA clone MGC:96884 cds. Gaps: Mismatches: Indels: Conservative: 143 0 0 PRI 08-MAR-2005

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Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting N Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor_Human Genome_Sequencing
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Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A.
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Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Baylor College of Medicine Human Genome
    (1-144)
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/codon startal
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HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGBEAMKKYSQILSHFEKLEPQAAVVK
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/tissue_type="PCR rescued clones"
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RS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Sanchez A, Whiting M, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodriguez KG, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MJ, Skalska U, Smailus DE, Schmerch A, Schein JE, Jones SJ and Marra MA.

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Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute,
                                                                                           Director MGC Project.
                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 9
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Room 11A03, Bethesda, MD
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(cDNA clone MGC:96896
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20892-2590,

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Pred. No.:
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    81
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Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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                                                                                                                                                          AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp
  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
                                                                     ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu
                                                                                                                                  GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC
                                                                                                                                                                                                                GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA
                                             AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC
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Gfseirgsvqakdgnidirilrrteslqdtkpanrccllrhllrlyldrvfknyqtpd
Hytlrkisslansfltikkdlrlchamtchcgeeamkkysqilshfeklepqaavvk
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/protein_id="AAH69559.1"
/db_xref="GI:47480992"
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/db_xref="MIM:605619"
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/clone="MGC:96896 IMAGB:7262105"
/tissue_typee="PCR rescued clones"
/clone_lib="NIH_MGC_244"
/note="Vector: pPCR-Script Amp SK(+)"
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|mol_type="mRNA"
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Mismatches:
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           GluGluThrGlu 144
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                                                                                       HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu
                                                                                                                 GAGGAGACAGAA
                                      GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG
                                                 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet
528
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Search completed: December 28, 2005, 12:45:48
Job time : 2950 secs

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Result
No.
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-MODBL=frame+ p2n.model -DEV=xlp
-MODBL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10789251/runat_23122005_152435_19737/app_query.fasta_1.327
-Q=/cgn2_1/USPTO_spool_p/US10789251/runat_23122005_152435_19737/app_query.fasta_1.327
-DB=N_Geneeeq -QEMT=fastap_-SUFFIX=p2n.rng_-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINHEN=0-1-2000000000
-USER=US10789251 @CGN 1 1 1096 @runat_23122005 152435 19737 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPDXT=0.5 -FGAPDP=6
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Maximum
                                                                                                                                                                                                                                                                                                                                                                        Database :
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                                                                                                                                                                                                                                              FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: geneseqn198
2: geneseqn200
3: geneseqn200
4: geneseqn200
5: geneseqn200
6: geneseqn200
7: geneseqn200
7: geneseqn200
10: geneseqn200
11: geneseqn20
11: geneseqn20
12: geneseqn20
13: geneseqn20
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Ygapop 10.0,
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Delop 6.0,
    100.0
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Adm95042 Human Int
Adv42800 Human psy
Aax77692 Human Zcy
Acf05161 Polynucle
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753 100.0 926 10 AAD61821 Aad61821 Human Cyt 753 100.0 926 12 AD980668 Ad980666 Human Zey 753 100.0 926 13 ADR34325 Add88066 Human Zey 753 100.0 926 13 ADR34325 Add88066 Human Zey 753 100.0 926 14 AEA50048 Ad98066 Human Zey 753 100.0 926 14 AEA50048 Ade820786 Human Cyt 753 100.0 926 14 AEA50048 Ade820786 Human Cyt 753 100.0 926 14 AEA50048 Ade1852 Human Cyt 753 100.0 926 14 AEA50048 Ade1852 Human Int 749 99.5 513 8 ABV75154 Ade28786 Ade1852 Human Int 749 99.5 867 6 AE074562 Ade1852 Human Int 749 99.5 867 6 AE074562 Ade1852 Human Int 749 99.5 925 12 ADN12153 Add115289 Human Int 749 99.5 925 12 ADN12153 Add115289 Add115289 Human Int 749 99.5 925 12 ADN12153 Add115289 Add115289 Human Int 749 99.5 925 12 ADN12153 Add115289 Add11528 Human PRO 7514 AEA50489 99.1 926 13 ADS31716 Add21715 Interleuk 7514 ADS31718 AAA512192 Add11528 Human PRO 7514 AAA5212192 Add11528 Human PRO 7514 AAA5212116 AAA646229 Human CDN 7514 AAA521216 AAA646229 Human CDN 7514 AAA521216 AAA646229 Human DNA 7514 AAA521216 AAA646229 Human PRO 7514 AAA521216 AAA646229 Human PRO 7514 AAA521216 AAA646229 Human DNA 7514 AAA521216 AAA646229 Human PRO 7514 AAA521216 AAA646229 Human PRO 7514 AAA62229 Add1154 Human PRO 7514 AAA62219 AAA646229 Human CDN 7514 AAA66603 AAA62219 Human PRO 7514 AAA62219 AAA62229 Human CDN 7514 AAA62219 AAA62229 Human CDN 7514 AAA62219 AAA62229 Human BRO 7514 AAA62213 AAA62229 Human BRO 7514 AAA6223 Human PRO 7514 AAA6223 AAA6223 Human BRO 7514 AAA6223 Human PRO 7514 AAA6223 Human PRO 7514 AAA6223 Human PRO 7514 AAA6223 Human PRO 7514 AAA6223 Human BRO 7514 AAA6233 Human BRO 7514 AAA623 Human BRO 7514 AAA623 Human BRO 7514 AAA623 Human BRO 7514 AAA623 Hum
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Query Match:
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          ADV42800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 528 BP;
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interleukin 2
                            ADV42800 standard;
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                                                                                                                   GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet
                                                                                                                                                                                              AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences up to SEQ ID NO 1829 are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing condition associated with PNI activity, e.g., inflammatory or
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              This invention describes a novel mammalian four alpha helix cytokine designated Zcytol0 which has vulnezary, cytostatic, anti-inflammatory, anti-asthmatic and haemostatic activity. Zcytol0 may be a growth and/or maintenance factor in the trachea and salivary glands, stomach, pancreas and muscle. Zcytol0 polynucleotides are useful as sources of primers and probes, and to determine if the Zcytol0 gene is present on chromosome 1, or to detect any mutations that may have occurred. Zcytol0 cor to detect any mutations that may have occurred. Zcytol0 cor to detect any mutations, and antibodies, as well as compounds cidentified as having binding affinity to Zcytol0, should be useful in the treatment of conditions associated with abnormal physiology or cor degenerative conditions or altered immunity. The products are also cuseful for modulating cell proliferation, cell differentiation or cytokine production in the prevention or treatment of conditions conditions associated with abnormal products are also cor degenerative conditions or altered immunity. The products are also cytokine production in the prevention or treatment of conditions conditions or altered immunity. The products are also cytokine products are also conditions conditions and antaconists may be a growth and be a products and antaconists may be a growth and be a product of the growth and antaconists may be a growth and antaconists may be a growth and be useful in the growth and antaconists may be a growth and be useful and be useful in the growth and antaconists may be a growth and antaconists may be a growth and be useful and b
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                                                                                                                                                                                                                                                                                                                       Polynucleotide encoding human interleukin-20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting the growth and/or proliferation of cervical cancer cells, useful for treating cervical cancer or human papilloma virus infection, comprises bringing Interleukin-20 (IL-20) into contact with the cervical cancer cells.
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Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopaenia; autoimmune disease; insulin-dependent diabetes mellitus; immune response; rheumatoid arthritis; multiple sclerosis; infection; radiation therapy; asthma; bronchitis; wound healing; periodontal disease; antiinflammatory; psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
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25-NOV-1998;
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Novel human cytokine-like polypeptide-10, 2cyto10, useful for treating insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, asthma, psoriasis and inhibiting cancer cell growth.

Disclosure; Col 29-30; ado English.

CC (Zcytold) polypeptide. Zcytold is useful for prevention or treatment of CC conditions characterised by improper cell proliferation, cell differentiation or cytokine production. Zcytold is useful for treating autoimmune diseases such as insulin-dependent diabetes mellitus, rehumatoid arthritis, multiple sclerosis, etc., by inhibiting cancer cell immune response. The invention is useful for inhibiting cancer cell growth or proliferation, for stimulating immune system to combat microbial or viral infections, for increasing platelet production, and thus useful in cancer patients who experience thrombocytopaenia due to cancer therapy or radiation therapy. Zcytold is useful in trachea-cc specific or tracheabronchial-specific applications, such as in the maintenance or would repair of the tracheabronchial epithelium or cells cunderlying the same, in regulating mucous production or mucocillary clearance of debris or in treatment of asthma, bronchitis or other diseases of the tracheabronchial tract. Zcytold may also enhance wound healing and promote regeneration of affected tissues which may be capacially useful in the treatment of periodontal disease. Zcytold can be useful to treat skin conditions such as sporiasis, eczema and dry skin in The invention relates to an isolated human cytokine-like polypeptide-10 Zcyto10 can be d\_dry skin in

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                                                                                                                        cytokine-like polypeptide-10; Zcytol0; wound healing; platelet proliferation; wound repair; mucous production, asthma; bronchitis; tracheobronchial tract disease; periodontal disease; skin condition; psoriasis; eczema; dry skin; protein therapy; human; vulnerary; respiratory; antibronchitic; dental; dermatological; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oral cavity and for modulating muscle tone in the tracheobronchial tract, and for treating muscle atrophy in the elderly, sick or bed-ridden. Zcytol0 is also useful for promoting wound healing. The present sequence is human Zcytol0 cDNA. The Zcytol0 gene is located on chromosome 10
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                                 "Human Zcytol0 protein"
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25-NOV-1998;
17-MAY-1999;
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AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp
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                                                                                                       GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC
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                                                                                                            New Zcyto10 polypeptides and polynucleotides, useful for treating autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
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P-PSDB; ADQ88067, ADQ88077, ADQ88091.
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25-NOV-1998;
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                                Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection; psoriasis; eczema; dry skin; wound healing; platelet proliferation;
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                                                                                                                                                                                                                                                                                                                           The invention relates to novel cytokine-like polypeptide-10 (Zcyto10) polypeptides and polynucleotides. Zcyto10 sequences are useful for treating asthma, microbial or viral infections, psoriasis, eczema or dry skin, for promoting the healing of wounds and for stimulating the proliferation of platelets. The present sequence is human Zcyto10 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated antibody that binds to a Zcytol0 polypeptide, treating asthma, microbial or viral infections, and for prohealing of wounds, psoriasis, eczema or dry skin.
                                                                                                                                                                                                                                                                                                         Sequence 926 BP; 258 A; 201
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          AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys
                                                 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu
                                                                              GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC
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CysVallleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer

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                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Classifying a breast cancer patient according to prognosis determining the similarity between the level of expression
                                                                                                                                                                                   No.:
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                                                                                                                                                     26-NOV-1997; 97US-0066597P
25-NOV-1998; 98US-00199586
15-APR-2003; 2003US-00413661
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AEA50048; 11-AUG-2005

Full length IL-20 coding sequence.

(first entry)

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a mammalian cytokine-like polypeptide, zcytol0 and its encoding polymucleotide. The invention is useful for modulating cell proliferation, cell differentiation or cytokine production in the prevention or treatment of conditions such as autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid arthritis, asthma or psoriasis) and cancer or wounds. The invention is also useful in gene therapy. The present sequence is the human zcytol0 protein encoding DNA. This Zcytol0 gene is located on chromosome 1q32.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that selectively binds to a ZcytolO polypeptide useful for modulating cell proliferation, cell differentiation or cytokine production in the prevention or treatment of e.g. autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 926 BP; 258 A; 201 C;
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P-PSDB; ADS18363, ADS18373.
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  standard;
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Alignment
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DB:
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Best Local Similarity:
                                                                                                                                                This sequence encodes full length interleukin-20 (IL-20), longer form IL-20 (20x1. The method of the invention for producing an antibody to IL-20 (comprises inoculating an animal with an IL-20 polypeptide which elicits an immune response in the animal to produce the antibody, and isolating the antibody from the animal. The antibody is useful for treating a CC pathological condition in a subject associated with IL-20 activity such as chronic inflammatory condition, specifically inflammatory bowel CC disease, ulcerative colitis. Crohns' disease, arthritis, atopic cendotoxemia, septicemia, toxic shock syndrome and infectious disease. An CC endotoxemia, septicemia, toxic shock syndrome and infectious disease. An inflammatory disease in which IL-20 plays a role such that the confident of IL-20 is useful for treating a mammal afflicted with an CC inflammatory disease in which IL-20 plays a role such that the Confident in the reduced, where the antagonist comprises an antibody, and conjugeptide that specifically binds a CC polypeptide or polypeptide tragment of IL-20, and where the inflammatory activity of IL-20, and untibody fragment, produced using the above method, binds to IL-20, and inhibits or reduces the pro-inflammatory CC antibody. The antibody or antibody fragment, produced using the above method, binds to IL-20, and inhibits or reduces the pro-inflammatory confidence or inhibited using the antibody.
                Y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; gene; Antiinflammatory; Gastrointestinal-Gen.; Antiulcer; Antiarthritic; Dermatological, Antipsoriatic; Antibacterial; Immunosuppressive; Antimicrobial; II-Antagonist-20; interleukin-20; IL-20; inflammation; inflammatory bowel disease; ulcerative colitis; Crohns disease; arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia; toxic shock syndrome; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful for treating inflammatory diseases e.g., Crohn's disease, by inoculation animal with the polypeptide eliciting an immune response to produce
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SR, Lehner JM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody production; cytokine; antiinflammatory; gastrointestinal-gen.; antiulcer; antiarthitic; dermatological; antipsoriatic; antibacterial; immunosuppressive; antimicrobial; inflammation; inflammatory bowel disease; ulcerative colitis; Crohns disease; inflammatory bowel disease; ulcerative colitis; crohns disease; arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis; arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis;
                                                                                                                                                                                                               21-NOV-2003;
24-MAR-2004;
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                                                                                         Kindsvogel WR, SR, Lehner JM,
                                                                                                                                                                   ZYMOGENETICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                         Hughes SD, Chandrasekher AW, Sivakumar PV, Moore M
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Producing an antibody to an interleukin 20RA (IL-20RA) polypeptide, useful for treating inflammatory diseases e.g., arthritis, by inoculating an animal with the polypeptide which elicits an immune response to produce the antibody.
       ID NO
1; 265pp; English.
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antiinflammatory, gastrointestinal-gen., antiulcer, antiarthritic, dermatological, antipsoriatic, antibacterial, immunosuppressive and antimicrobial applications. The antibacterial was be useful for treating a pathological condition in a subject associated with II-20RA, such as a chronic inflammatory condition selected from inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis and psoriasis, cancer, or an acute inflammatory condition such as endotoxemia, septicemia, toxic shock syndrome and infectious disease. The content sequence is that of a human II-20 precursor cDNA clone of the The invention relates to a novel method for producing an antibody to a polypoptide. The method comprises inoculating an animal with a polypoptide selected from any of SEQ ID NO: 14, 15, 17 or 19 as given in the specification, where the polypoptide elicits an immune response in the animal to produce the antibody, and isolating the antibody from the animal. The antibody specifically binds to the pro-inflammatory cytokine interleukin 20 (IL-20 or Zcytol0), or one its receptors IL-20RA (ZcytpR?) or IL-20RB (DDIRS1). The method of the invention demonstrates The

Sequence 926 BP; 258 A; 201 C; 187 G; 280 Η, 0 U; 0 Other;

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
14	100.00%	100.00%	100.00%	753.00	1.17e-86	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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-01-SD 789-251-26 (1-144) x AEA28786 (1-926)

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                                                                                                                                                     AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys
                                                                                                                                                                                                         ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu
                                                                                                                                                                                                                                                                                                          ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln
GluGluThrGlu 144
                                  GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGGAACTAGACATTCTTCTGCAATGGATG
                                                                                      CATTGTGGGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
                                                                                                  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu
                                                                                                                                       GCCAATTCCTTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC
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13-APR-2001; 2001US-0283688P 12-APR-2002; 2002WO-US011513 WO200283853-A2 Protein synthesis; data mining; recombinant; interleukin-20; IL-20; human; ds. Human interleukin-20 19-FEB-2003 24-OCT-2002 ABV75151; (first entry) (IL-20)codon optimised fragment zcyto10X1.

WPI; 2003-067576/06. Pownder TA, Chan C; (ZYMO ) ZYMOGENETICS INC.

New polynucleotide, useful for producing a nucleic acid construct expression of an amino acid sequence of interest. for

Example 1; Page 36; 40pp; English.

CC The invention provides a new purified polynucleotide that comprises the nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide code sequence of 13 nucleic acids, where the sequence has homology with 13 CC base pair (bp) sequence, where at least 5 nucleic acids are identical to CC a 13 bp sequence (ABV75139), and where the nucleic acids sequence does not CC code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16 CC or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide cCC sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected from 9 sequences (ABV75144-150) where at least 50% nucleotides are either CC polynucleotide is useful for producing a nucleic acid construct for capression of an anino acid sequence of interest. The present sequence CC represents a human interleukin-20 (IL-20) codon optimised fragment for CC expression in E. coli

Sequence 462 BP; 121 A; 131 Ç 117 <u>ن</u> 93 H. 0 Ġ, 0 Other;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                   No.:
1.38e-86
749.00
100.00%
99.31%
99.47%
8
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
143
0
0
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US-10-789-251-26 (1-144) x ABV75151 (1-462)

RESULT 13 ABV75151 ID ABV75

ABV75151

standard; DNA; 462 BP

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RESULT 14
ARB26649
ID ARB266
XX ARB26
XX ARB26
XX DH Human
XX Expre
XX Expre
XX CDS
FT CDS
FT CDS
FT CDS
FT 10-D1
XX HODO
XX WO20(
XX WD1)
PF 10-D1
XX I2-D1
XX I2-D1
XX PP CONT
PR P-PS
XX WP1;
DR P-PS
XX WP1;
DR P-PS
XX New
PT CONT
PS Exam
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                                                                                The invention relates to Syn 1 and Syn 2 tight regulated synthetic promoters and methods for enhancing the expression of recombinant proteins. The Syn 1 and Syn 2 tight regulated synthetic promoters are useful for controlling uninduced, leaky expression of proteins that are toxic and interfere with production of recombinant protein from an Escherichia coli expression system. They are useful for controlling basal expression of target genes. The present sequence is the human interleukin (II) 20 DNA. This sequence is used in the comparison of promoter
                                               Sequence
                                                                                                                                                                                                                                  New Syn 1 and Syn 2 tight regulated synthetic promoters, useful for controlling uninduced, leaky expression of proteins that are toxic and interfere with production of recombinant protein from an Escherichia coli
                                                                                                                                                                                              Example 5; SEQ ID NO 18; 39pp; English.
                                                                                                                                                                                                                        expression
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                                                 462
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                           New polynucleotide, useful for producing a nucleic acid expression of an amino acid sequence of interest.
                                                                                                Pownder TA,
                                                                                                                                                      13-APR-2001; 2001US-0283688P
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                                                                                                                                                                                                                                                                                Synthetic
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Example 1; Page 37; 40pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a new purified polynucleotide that comprises the CC nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide CC sequence of 13 nucleic acids, where the sequence has homology with 13 CC base pair (bp) sequence, where at least 5 nucleic acids are identical to a 13 bp sequence (ABV75139), and where the nucleic acids sequence does not CC code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16 CC or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide cCC from 9 sequences (ABV75141), E= polynucleotide sequence selected cCC from 9 sequences (ABV75144-150) where at least 50% nucleic des are either CC adenine or thymine, and where only E encodes a stop codon. The CC polynucleotide is useful for producing a nucleic acid construct for CC expression of an amino acid sequence of interest. The present sequence CC represents a sequence comprising an expression cassette (EC) cc polynucleotide sequence inserted upstream of a human interleukin-20 (IL-CC) ccdon optimised fragment for expression in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 513 BP; 143 A; 145 C; 126 G; 99 T; 0 U; 0 Other;
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                                                                                                 GAACCGCAGGCAGCAGTGGAAAGCTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG
                                                                                                                                GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
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